

codespaces_RStudio



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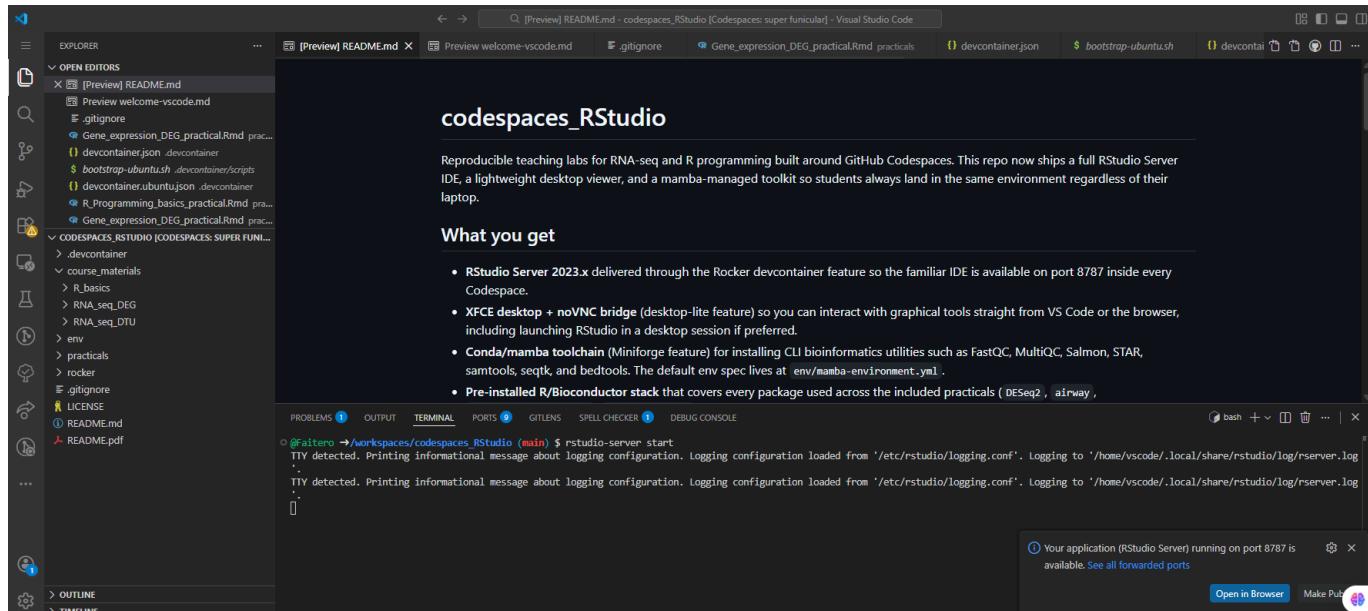
Reproducible teaching labs for RNA-seq and R programming built around GitHub Codespaces. This repo ships a full RStudio Server IDE, an optional desktop-lite workflow, and a mamba-managed toolkit so every student lands in the same environment regardless of their laptop.

Launch a brand-new Codespace

1. Click **Open in GitHub Codespaces**. GitHub provisions a Codespace from `.devcontainer/devcontainer.json`.
2. Initial creation installs Ubuntu packages, R/Bioconductor libraries, and CLI tools. Plan for **30 minutes**. Keep the tab open until the build completes.
3. Once VS Code opens, run:

```
rstudio-server start
```

4. Port **8787** auto-forwards. Use the notification or Ports tab to open RStudio (user `rstudio`, password `rstudio`).



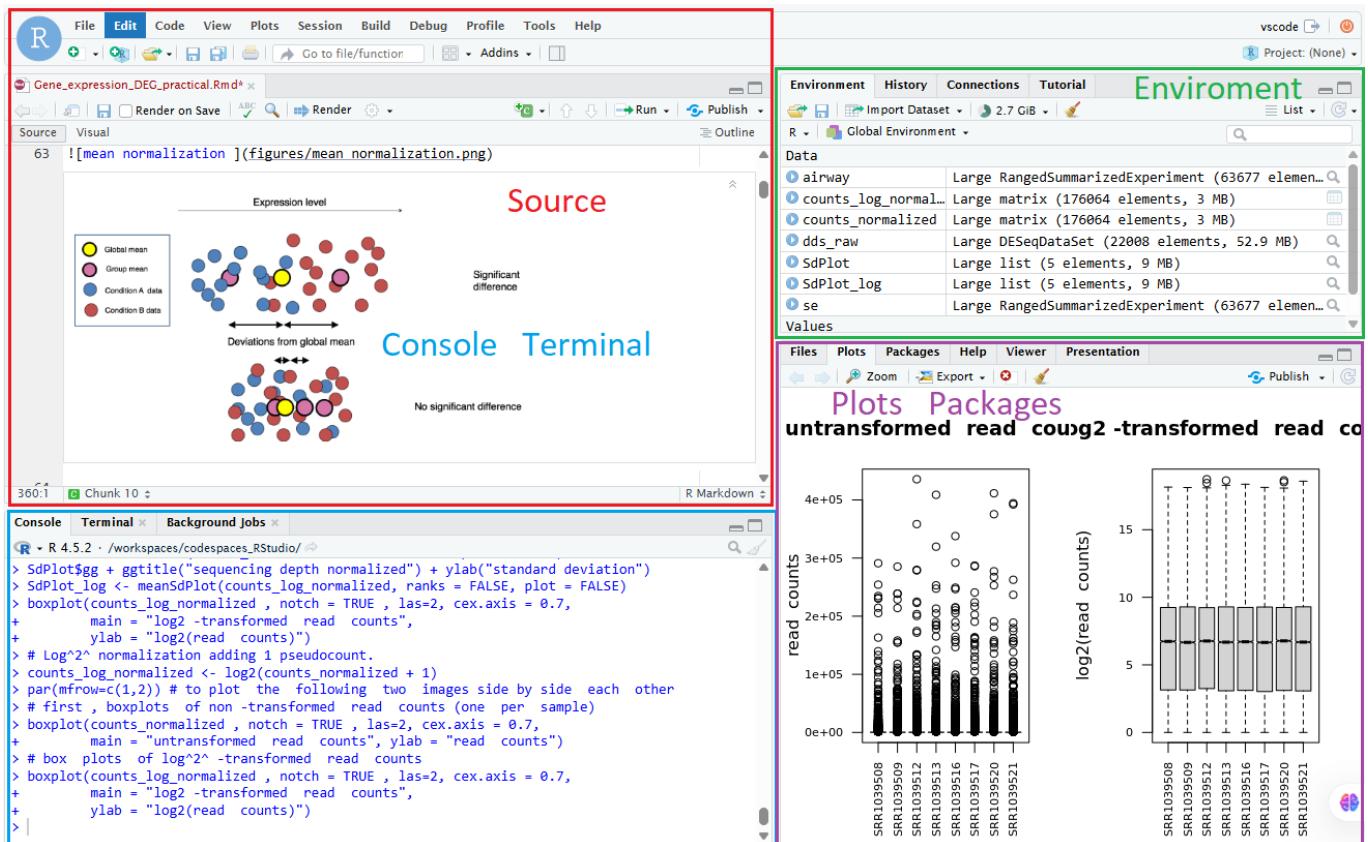
Resume an existing Codespace

1. Click **Reopen My Codespace** button on top and pick the workspace you created earlier.
2. Because packages are already cached, it resumes in seconds.
3. Restart RStudio with `rstudio-server start` and reopen port 8787.

RStudio IDE overview

A screenshot annotated with these callouts will be inserted here.

- **Source** edit R scripts/Rmd notebooks, run chunks, and view rendered docs.
- **Console** executes commands interactively; shows warnings/errors and `rstudio-server` messages.
- **Terminal** full shell access (bash) for mamba commands, git, or custom scripts.
- **Environment** lists objects currently in memory (data frames, vectors, models); lets you inspect or remove them.
- **History** chronological log of executed commands with buttons to re-run or send to Source.
- **Files** browse project folders, upload/download files, and open notebooks.
- **Plots** displays the current graphics device; use navigation arrows to flip through prior plots.
- **Packages** see installed libraries, enable/disable them, and launch help pages.



Quick start in RStudio

1. Open the `.Rmd` you want (see **Lessons** below) via the Files pane.
2. Set the working directory with `setwd()` or the gear icon if needed.
3. Use **Run** / **Run All** buttons to execute chunks, or press **Ctrl+Shift+Enter** (**Cmd+Shift+Enter** on macOS) to knit.
4. Keep an eye on the Console for errors; restart R (`Session` → `Restart R`) if memory gets cluttered.

Lessons in `practicals/`

1. **R_Programming_basics_practical.Rmd** introduces R syntax, data frames, and visualization fundamentals tailored for bioinformatics students.
2. **Gene_expression_DEG_practical.Rmd** walks through differential gene expression analysis with DESeq2, including QC, normalization, and volcano plots.

3. **DEXSeq_salmon_DTU_practical.Rmd** covers isoform-level quantification with Salmon and DEXSeq for differential transcript usage.

What you get

- **RStudio Server 2023.x** exposed on port 8787 via the Rocker devcontainer feature.
- **Xfce desktop + noVNC bridge** (desktop-lite feature) so you can run GUI apps inside the Codespace when enabled.
- **Conda/mamba toolchain** (Miniforge feature) for FastQC, MultiQC, Salmon, STAR, samtools, seqtk, bedtools, etc. ([env/mamba-environment.yml](#)).
- **Pre-installed R/Bioconductor stack** covering all supplied practicals (DESeq2, airway, IsoformSwitchAnalyzeR, clusterProfiler, ...).
- **Ready-to-teach content:** Rmd notebooks, docs, and data mirrored from the original Gitpod-based course.

Repository layout

- [docs/](#) grading material and supporting markdown.
- [env/](#) shared config such as [mamba-environment.yml](#) and R data sets.
- [figures/](#) reference screenshots.
- [rocker/](#) legacy Dockerfiles.
- [*.Rmd](#) the teaching notebooks students run in RStudio.

Pre-installed R packages

The post-create hook runs [.devcontainer/scripts/install-r-packages.R](#), ensuring:

- airway, SummarizedExperiment, DESeq2, vsn, apeglm, AnnotationDbi, org.Hs.eg.db
- clusterProfiler, enrichplot, DOSE, IsoformSwitchAnalyzeR
- tidyverse, ggplot2, ggnewscale, ggbeeswarm, ggrepel, pheatmap, RColorBrewer, dbplyr, tidyr, readr, GGally Add more via that script as needed.

Local VS Code / Dev Container usage

```
# Requires Docker + VS Code Dev Containers extension
git clone https://github.com/FairTeach/codespaces_RStudio.git
cd codespaces_RStudio
code .
# When prompted, "Reopen in Container"
```

Same devcontainer features run locally, so behavior matches Codespaces.

Managing CLI dependencies with mamba

Miniforge installs mamba under [/opt/conda](#). The bootstrap script creates/updates [rnaseq-tools](#) defined in [env/mamba-environment.yml](#):

```
mamba activate rnaseq-tools  
multiqc --help
```

Add extra tools (e.g., gffcompare, bwa, hisat2) to the YAML and rebuild or run `mamba env update` inside the Codespace.

Troubleshooting tips

- Rebuild the container ([Codespaces / Rebuild container](#)) after changing `.devcontainer/**`, `env/mamba-environment.yml`, or bootstrap scripts.
- If RStudio Server doesn't start, check the Ports tab for 8787; restart with `rstudio-server stop` / `rstudio-server start`.
- Desktop-lite can be toggled via the command palette ([Codespaces: Open in Browser](#)) if you need the VNC desktop.

Happy learning? Questions or suggestions? Open an issue or reach out on @FairTeach!

Contact and Support

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